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What is claimed is:

1. L-Lysine-producing corynebacteria with an enhanced lysE gene, in which additionally genes selected from the group consisting of the dapA gene, the lysC gene, the pyc gene and the dapB gene, individually or together, are enhanced.

2. Corynebacteria as claimed in claim 1 in which the dapB gene is enhanced.

3. Corynebacteria as claimed in claim 1 in which the dapB gene, which additionally contains the 5′ end upstream from the translation start of this gene, said 5′ end being shown in SEQ ID No. 1, is enhanced.

4. Corynebacteria as claimed in claim 1 which contain the MC20 or MA16 mutation of the dapA promoter shown respectively in SEQ ID No. 5 and SEQ ID No. 6.

5. Isolated DNA originating from Corynebacterium and capable of replication in corynebacteria, which contains at least the nucleotide sequence coding for the 5′ end upstream from the translation region of the dapB gene, shown in SEQ ID No. 1.

6. DNA capable of replication, as claimed in claim 5, comprising the nucleotide sequence shown in SEQ ID No. 1.

7. Corynebacteria as claimed in claim 1 in which the dapA gene and the lysC gene are enhanced.

8. Corynebacteria as claimed in claim 1 wherein the genes are enhanced through over-expression.

9. Corynebacteria as claimed in claim 2 wherein the dapB gene is over-expressed.

10. Corynebacteria as claimed in claim 3 wherein the dapB gene is over-expressed.

11. The DNA of claim 5 which is recombinant.

12. Escherichia coli K-12 strain DH5α/pEC7dapBlysE, deposited as DSM12875.

13. Corynebacterium glutamicum strain DSM5715aecD::dapA(MA16), deposited as DSM12867.

14. Corynebacterium glutamicum strain DSM5715aecD::dapA(MC20), deposited as DSM12868.